

WRKY TRANSCRIPTION FACTOR IN SUGARCANE DEFENCE AGAINST COLLETOTRICHUM FALCATUM

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Transcription factor, a key regulatory element for gene expression present in all organisms. WRKY is one amongst 10 largest transcription factor families present, which is plant-specific, however reported in protists, slime mold and pine. WRKY TF's play key regulatory role in signalling pathways associated with various environmental stresses inclusive of pathogen interaction. During host-pathogen interaction, transcriptional control of a gene expression by up or down regulation results in resistance and susceptibility of the host to invading pathogen.

WRKY transcription factor functions as an important element in the complex signaling pathways in plants during incompatible interaction against pathogen. In *Hordeum vulgare* HvWRKY 1 and HvWRKY 2 act as negative regulators in the effector triggered immunity against powdery mildew (*Blumeria graminis* f.sp. *hordei*) (Rushton et al., 2010). Also, in rice WRKY45 TF plays a crucial role in salicylic acid (SA)/benzothiadiazole (BTH)-induced disease resistance to fungal pathogen *Magnaporthe oryzae* and bacterial pathogen *Xanthomonas oryzae*pv. *oryzae* (Nakayama et al., 2013).

WRKY role in senescence was studied using *Arabidopsis thaliana* mutants were AtWRKY 6 regulates SIRK (Senescence induced receptor kinase). Mitogen activated protein kinase (MAPK) pathway in *Arabidopsis* controls WRKY during pathogen defense. AtWRKY 33 form complex with MAP kinase followed by activation of PAD3 (Phytoalexin deficient 3) which synthesis antimicrobial camalexin. It involved in auto regulation by regulating its own promoters or cross regulating other transcription factor family members (Rushton et al., 2010). WRKY transcription factor involved in various regulatory process are studied in many plants

In sugarcane, redrot is a major disease caused by *Colletotrichum falcatum* Went which infects cane stalks. The infected stalks become unfit for milling and quality of juice is affected due to inversion of glucose and fructose. The function of WRKY TF's in defense is proven as several EST-contigs were identified. Also a ScWRKY gene was identified for its active role in defence response against *Sporisorium scitamineum*, salicylic acid, drought and salinity (Liu et al., 2012). Among five different transcription

factors studied in sugarcane during *C. falcatum* interaction, WRKY showed differential expression pattern in resistant and susceptible varieties (Muthumeena et al., 2013). In continuation of the previous studies, we have taken up detailed studies to identify active involvement of WRKY TF's during sugarcane and *C. falcatum* interaction.

A total of 36 ScWRKY sequences were retrieved and primers were designed using FastPCR tool (Ver. 3.6.62). Expression analyses were performed with the sugarcane cultivars Co 93009(R) and CoC 671(S) which were inoculated with *C. falcatum* pathotype Cf671 conidial suspension ($1 \times 10^6 / \text{mL}^{-1}$) and the samples were collected at 0, 6, 12, 24, 36, 48 and 72h later. RNA was isolated from the samples and expression studies were taken up by RT-PCR.

Among the 36 ScWRKY primers, 16, 18, 19, 26, 31 and 35 primers showed expression and they were further used to study the spatial and temporal expression pattern during

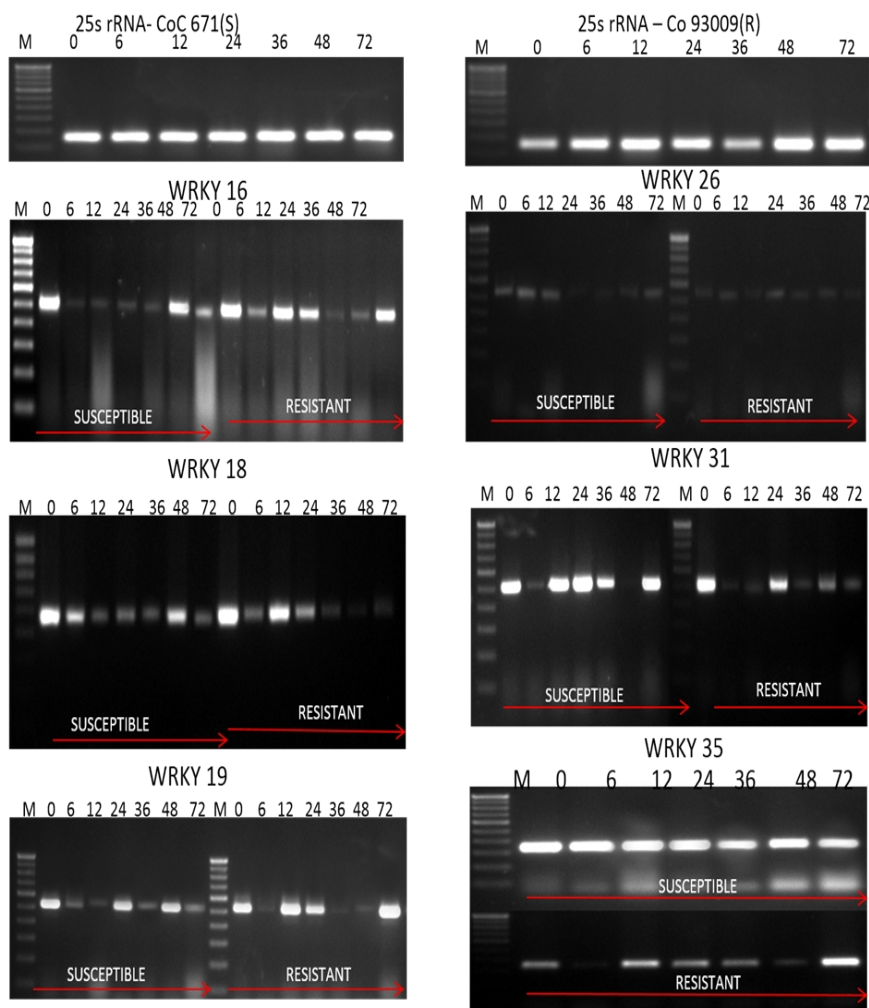


Fig. 1. Differential expression of ScWRKY transcription factors

C. falcatum interaction with sugarcane. WRKY 16, 18 and 19 showed higher expression in susceptible cultivar at 48h where as it was expressed low in other intervals. However the resistant cultivar showed early and late induction. WRKY 26 expressed in early stages in both susceptible and resistant samples. Also WRKY 31 and 35 showed high expression in the susceptible cultivar compared to the resistant cultivar (Fig. 1).

Further studies are being continued to identify specific expression of resistance associated transcription factor in WRKY family and their relation to expression of genes involved in defence related signal transduction pathway.

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